REMARKS

Claims 1, 2, and 39-41 are pending. In the Office action mailed May 14, 2010, claims 1, 2, and 39-41 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite. Claims 1, 2, 40, and 41 are rejected under 35 U.S.C. § 103(a) as being unpatentable over Houstek et al., Hum Mol Genet 8:1967-74, 1999 ("Houstek") in view of PCT Publication WO 95/11995 ("Chee"). Claim 39 is rejected under 35 U.S.C. § 103(a) as being unpatentable over Houstek and Chee in view of U.S. Patent 5,541,308 ("Hogan"). Claims 1, 40, and 41 are also rejected under 35 U.S.C. § 103(a) as being unpatentable over Rustin et al., Biochim Biophys Acta 1553:117-22, 2002 ("Rustin") in view of Chee. Claim 39 is also rejected under 35 U.S.C. § 103(a) as being unpatentable over Rustin and Chee in view of Hogan. Each of these rejections is addressed below.

Claim amendments

Claim 1 has been amended to recite that the nucleic acid molecules or nucleic acid molecule fragments are wild-type sequences, i.e., not mutant sequences. Support for this amendment is found, for example, at page 25, lines 11-13. Claim 2 has been amended to remove parenthetical references where appropriate.

These amendments add no new matter.

Rejection under 35 U.S.C. § 112, second paragraph

Claims 1 and 2 are rejected as being indefinite. Each of these rejections is addressed below.

Claim 1 is rejected for reciting a microarray that "consists of" nucleic acid molecules, on the ground that this claim requires a microarray to be limited to nucleic acid molecules without any solid support. Applicants respectfully traverse.

As an initial matter, Applicants note that claim 1 previously recited a solid support. As explained on page 5 of their April 7, 2009 reply, Applicants deleted this language

from claim 1 based upon the Office's suggestion. Applicants are thus surprised to learn that the language suggested by the Office is now being rejected as indefinite. In addition, the definition of "microarray" (starting at page 18, line 21 of the specification) indicates that a microarray includes nucleic acid molecules or polypeptides affixed to a solid support. As a "microarray" necessarily includes a solid support, it is unnecessary, and indeed would be redundant, for claim 1 also to recite a solid support. The language of claim 1 is definite.

Claim 2 is rejected as being indefinite for reciting a name and then a name within parentheses. The Office takes the position that the parenthetical references make the claim indefinite because it is unclear whether the information in the parentheses has the same, less, or more weight than the rest of the claim. Without assenting to this rejection, Applicants have amended claim 2 to remove parenthetical references except where the gene name itself contains a parenthetical reference ("cytochrome c oxidase subunit VIIa polypeptide 2 (liver)," Exhibit A; "NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex 1, 8kDa," Exhibit B).

Withdrawal of the § 112, second paragraph, rejections is respectfully requested.

Rejection under 35 U.S.C. § 103(a) – Houstek in view of Chee

Claims 1, 2, 40, and 41 are rejected as being obvious over Houstek in view of Chee. In making this rejection, the Office cites Houstek as teaching screening of nuclear ATPase subunits to determine the location of a mutation. The Office concludes that this disclosure provides a reason to use a composition consisting of nuclear genes. Houstek, however, does not teach a microarray. To overcome the deficiency of Houstek, the Office cites Chee as teaching a tiling microarray that can be used to identify mutations in a sequence. Applicants respectfully traverse.

Contrary to the Office's position, Houstek does not provide motivation to screen only nuclear genes, and in this respect is cumulative with the references previously cited

by the Office. As explained in the second paragraph of Houstek, the ATPase subunits include both nuclear and mitochondrial genes. Thus, one seeking to identify mutations in the ATPase subunits would not exclude mitochondrial genes from analysis, because an ATPase defect in any given patient may result from a mutation in either the mitochondrial or nuclear DNA. Indeed, Houstek takes exactly this approach. Houstek explains (page 1969, left column, third full paragraph) that analysis was first performed on the subject's mitochondrial DNA (mtDNA) and that this analysis failed to find deletions, rearrangements, or the presence of common mutations. Only then did Houstek test the possibility that the observed ATPase defect was nuclear in origin. Thus, Houstek explicitly teaches analysis of both mitochondrial and nuclear DNA, teachings directly contrary to the Office's position. For this reason, Houstek cannot form the basis for rendering claim 1 or its dependent claims obvious.

Further, this deficiency of Houstek is not remedied by Chee, which is concerned solely with microarrays capable of identifying variants of a reference sequence (page 2, line 29, to page 3, line 5, of Chee). Like Houstek, Chee provides no suggestion to analyze only nuclear genes of the mitochondrial respiratory chain and, if anything, suggests the opposite. Chee instead notes that microarrays containing mitochondrial DNA would be useful for diagnosis of diseases (see, e.g., page 104, line 12-33) as well as for other purposes. Because neither Houstek nor Chee teaches or suggests a microarray that focuses solely on nuclear-encoded genes of the mitochondrial respiratory chain, this combination of references fails to teach all limitations of claim 1. For this reason, the combination of Houstek and Chee cannot render claim 1 or its dependent claims obvious.

In addition, Houstek does not suggest identifying mutations through use of a microarray. As explained on page 1973, Houstek uses a variety of techniques, including DNA isolation, electrophoresis, Southern hybridization, PCR, cloning, and sequence analysis, to analyze DNA sequences. There is no suggestion in Houstek to analyze DNA using a microarray.

This deficiency is also not remedied by Chee because this reference also fails to suggest analysis of nuclear encoded genes of the mitochondrial respiratory chain using a microarray. Thus, there is nothing in either of these references that would lead the skilled artisan to combine the genes of Houstek with the microarrays of Chee. For this reason as well, Houstek and Chee cannot render claim 1 or its dependent claims obvious.

Finally, Applicants note that claim 1 has been amended to require that the nucleic acid molecules of the microarray are *wild-type* nucleic acid molecules. As explained above, Chee teaches microarrays containing a substantial number of mutant sequences, and Houstek does not teach a microarray at all. Thus, neither Chee nor Houstek teaches or suggests a microarray where 90% of the nucleic acids molecules are wild-type nucleic acid molecules or fragments thereof. Accordingly, no combination of these references can render claim 1 or its dependent claims obvious.

Because these references fail to teach or suggest the microarray of claim 1, withdrawal of the § 103(a) rejection over Houstek in view of Chee is respectfully requested.

Rejection under 35 U.S.C. § 103(a) - Houstek and Chee in view of Hogan

Claim 39 is rejected as being obvious over Houstek and Chee in view of Hogan. Houstek and Chee are cited for the reasons set forth above. However, Houstek and Chee do not teach nucleic acid fragments at least 40 nucleotides in length, as required by claim 39. To provide this teaching, the Office cites Hogan as teaching probes that are 15-50 nucleotides in length. Based on this combination of references, the Office concludes that claim 39 is obvious.

Applicants respectfully traverse this rejection for the reasons set forth above. As explained above, neither Houstek nor Chee suggest excluding mitochondrial genes from analysis. In addition, both Houstek and Chee fail to teach the use of microarrays to analyze nuclear encoded genes of the mitochondrial respiratory chain at all. Finally, as

explained above, claim 1 has been amended to recite a microarray that includes *wild-type* sequences, a limitation neither taught nor suggested by Chee or Houstek.

Hogan fails to overcome these deficiencies and is instead focused on detection of ribosomal RNA. Like Houstek and Chee, Hogan does not suggest analyzing only nuclear encoded genes of the mitochondrial respiratory chain. Indeed, Hogan does not suggest analysis of nuclear encoded genes of at all, and thus cannot teach or suggest making a microarray consisting of such genes. Accordingly, no combination of Houstek, Chee, and Hogan teaches or suggests the present invention. These references therefore cannot render the present claims obvious.

Withdrawal of the § 103(a) rejection over Houstek and Chee in view of Hogan is respectfully requested.

Rejection under 35 U.S.C. § 103(a) - Rustin in view of Chee

Claims 1, 2, 40, and 41 are also rejected as being obvious over Rustin in view of Chee. In making this rejection, the Office cites Rustin as suggesting the use of probes for detection of mutations in complex II. Because complex II consists of only nuclear genes, the Office contends that it would be obvious to use probes that consist of only nuclear genes. Chee, as above, is cited as teaching a tiling microarray capable of detecting mutations. Based on this combination of references, the Office concludes that it would be obvious to make a microarray consisting of complex II genes, based on Rustin, using the design constraints of Chee. Applicants respectfully traverse this rejection.

While Rustin focuses on mitochondrial defects in complex II and describes a number of references in which mutations in complex II genes were identified, like Houstek, Rustin provides no basis for studying complex II mutations using microarrays. Indeed, references that are cited in Rustin, such as Baysal et al. (Science 287:848-51, 2000), describe identification of complex II mutations through direct sequencing. Thus, there is nothing in Rustin to suggest microarray-based analysis of complex II genes.

Chee fails to overcome the deficiency of Rustin. As explained above, Chee teaches microarrays capable of identifying variants of a reference sequence but provides no suggestion to analyze nuclear genes of the mitochondrial respiratory chain using such an approach. If anything, Chee suggests the opposite, i.e., that microarrays containing mitochondrial DNA would be valuable (see, e.g., the section of Chee starting at page 103, line 20). Absent such a teaching, these references fail to teach or suggest all limitations of claim 1. Thus, Rustin and Chee cannot render claim 1 or its dependent claims obvious.

Further, as noted above, claim 1 has been amended to recite *wild-type* nucleic acid molecules or fragments, a limitation neither taught nor suggested by either Rustin or Chee. Rustin is focused on identification of mutations in complex II, and Chee is focused on microarrays capable of detecting mutations using probes having mutations. Accordingly, no combination of these references would lead the skilled artisan to a microarray that includes primarily wild-type sequences. For this reason as well, Rustin and Chee cannot render claim 1 or its dependent claims obvious.

Because no combination of Rustin and Chee teaches or suggests the microarray of claim 1, these references cannot render claim 1 or its dependent claims obvious. Withdrawal of the § 103(a) rejection over Rustin and Chee is accordingly requested.

Rejection under 35 U.S.C. § 103(a) - Rustin and Chee in view of Hogan

Claim 39 is rejected as being obvious over Rustin and Chee in view of Hogan. As above, the Office cites Rustin and Chee as suggesting a microarray consisting of nucleic acid fragments of nuclear genes of complex II. However, Rustin and Chee do not teach nucleic acid fragments at least 40 nucleotides in length, as required by claim 39. To provide this teaching, the Office again cites Hogan and concludes that the combination of Rustin, Chee, and Hogan renders claim 39 obvious. Applicants respectfully traverse this rejection.

As explained above, Rustin and Chee do not teach or suggest a microarray for analyzing nuclear encoded mitochondrial respiratory chain genes. Nor do these references suggest a microarray containing primarily wild-type sequences. Hogan fails to overcome either of these deficiencies.

As explained above, Hogan is focused on detection of ribosomal RNA. Hogan thus does not teach or suggest a microarray for analyzing nuclear-encoded mitochondrial respiratory chain genes, either alone or in combination with Rustin and Chee. Accordingly, no combination of these references teaches or suggests the microarray of the present invention. These references therefore cannot render claim 39 obvious.

Withdrawal of the § 103(a) rejection over Rustin and Chee in view of Hogan is respectfully requested.

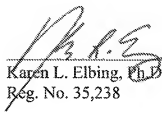
CONCLUSION

Applicants submit that the claims are in condition for allowance, and such action is respectfully requested. Enclosed is a Petition to extend the period for replying to the Office action for two (2) months, to and including October 14, 2010.

If there are any additional charges or any credits, please apply them to Deposit Account No. 03-2095.

Respectfully submitted,

Date: 14 October 2010



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Telephone: 617-428-0200
Facsimile: 617-428-7045

Entrez Gene

Genes and mapped phenotypes

Display Settings: Full Report

COX7A2 cytochrome c oxidase subunit VIIa polypeptide 2 (liver) [*Homo sapiens*]

Gene ID: 1347, updated on 12-Aug-2010

Summary

Official Symbol	COX7A2 provided by HGNC
Official Full Name	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) provided by HGNC
Primary source	HGNC:2288
See related	Ensembl:ENSG00000112695; HPRD:00482; MIM:123996
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	VIIAL; COX7AL; COX7AL1; COXVIIAL; COXVIIa-L; MGC118950; MGC118951; MGC118952; MGC126875; MGC126877; COX7A2
Summary	Cytochrome c oxidase, the terminal component of the mitochondrial respiratory chain, catalyzes the electron transfer from reduced cytochrome c to oxygen. This component is a heteromeric complex consisting of three catalytic subunits encoded by mitochondrial genes, and multiple structural subunits encoded by nuclear genes. The mitochondrially-encoded subunits function in electron transfer, while the nuclear-encoded subunits may function in the regulation and assembly of the complex. This nuclear gene encodes polypeptide 2 (liver isoform) of subunit VIIa, with this polypeptide being present in both muscle and non-muscle tissues. In addition to polypeptide 2, subunit VIIa includes polypeptide 1 (muscle isoform), which is present only in muscle tissues, and a related protein, which is present in all tissues. Alternative splicing results in multiple transcript variants. Related pseudogenes have been identified on chromosomes 4 and 14. [provided by RefSeq]

Genomic regions, transcripts, and products

(minus strand) Go to reference sequence details — Go to nucleotide graphics

Genomic context

chromosome: 6; Location: 6q12 — See COX7A2 in MapViewer

Bibliography

Related articles in PubMed

1. Polymorphisms in mitochondrial genes and prostate cancer risk. Wang L, *et al.* Cancer Epidemiol Biomarkers Prev. 2008 Dec. PMID 19064571.

Exhibit A

2. Identification of intrahepatic cholangiocarcinoma related genes by comparison with normal liver tissues using expressed sequence tags. Wang AG, *et al.* Biochem Biophys Res Commun, 2006 Jul 7. PMID 16712791.
3. The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC). Gerhard DS, *et al.* Genome Res, 2004 Oct. PMID 15489334.
4. The DNA sequence and analysis of human chromosome 6. Mungall AJ, *et al.* Nature, 2003 Oct 23. PMID 14574404.
5. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. Strausberg RL, *et al.* Proc Natl Acad Sci U S A, 2002 Dec 24. PMID 12477932.

See all (13) citations in PubMed

GeneRIFs: Gene References Into Functions What's a GeneRIF?

1. Observational study of gene-disease association. (HuGE Navigator)

Submit: New GeneRIF Correction

General gene information

Markers

WI-20346 (e-PCR)
Links: UniSTS:3346
NoName (e-PCR)
Links: UniSTS:489009
D4S3276 (e-PCR)
Links: UniSTS:79212
NoName (e-PCR)
Links: UniSTS:484221
RH41034 (e-PCR)
Links: UniSTS:85640

Genotypes

See COX7A2 SNP Geneview Report
See COX7A2 SNP Genotype Report

Related pseudogene(s)

2 found Review record(s) in Gene

Homology

Map Viewer (Mouse)

Pathways

KEGG pathway: Alzheimer's disease
05010
KEGG pathway: Cardiac muscle contraction
04260
KEGG pathway: Huntington's disease
05016
KEGG pathway: Oxidative phosphorylation
00190
KEGG pathway: Parkinson's disease
05012

Gene Ontology provided by GOA

Function	Evidence	
	Evidence Code	Pubs
cytochrome-c oxidase activity	IEA	
electron carrier activity	IEA	

Component	Evidence	
	Evidence Code	Pubs
membrane	IEA	
mitochondrial respiratory chain	IEA	

mitochondrion	IEA	

General protein information

Preferred Names
cytochrome c oxidase subunit 7A2, mitochondrial

Names
cytochrome c oxidase subunit 7A2, mitochondrial
OTTHUMP00000016749
OTTHUMP00000016750
OTTHUMP00000220651
OTTHUMP00000220652
OTTHUMP00000220653
OTTHUMP00000220654
cytochrome c oxidase subunit VIIaL
cytochrome c oxidase subunit VIIa-L
hepatic cytochrome-c oxidase chain VIIa
cytochrome c oxidase subunit VIIa-liver/heart
cytochrome c oxidase polypeptide VIIa-liver/heart
cytochrome c oxidase polypeptide 7A2, mitochondrial

NP_001856.1
EC 1.9.3.1

NCBI Reference Sequences (RefSeq)

RefSeqs maintained independently of Annotated Genomes

These reference sequences exist independently of genome builds. Explain

mRNA and Protein(s)

1. NM_001865.3 → NP_001856.2 **cytochrome c oxidase subunit 7A2, mitochondrial precursor**

Description	Transcript Variant: This variant (1) represents the shorter transcript but encodes the functional protein.
Source sequence(s)	AA878033,BC101826,CK821341
Consensus CDS	CCDS34486.1
UniProtKB/Swiss-Prot	P14406
Related Ensembl	ENSP00000230459, ENSP00000359098, ENSP00000359106, ENSP00000421193, ENSP00000378736, ENSP00000422979, ENSP00000423432, ENSP00000425951, ENST00000230459, ENST00000370081, ENST00000370089, ENST00000377978, ENST00000393013, ENST00000459637, ENST00000460985, ENST00000472311, ENST00000509698

Conserved Domains (1) summary

cd09928 Location:56 – 110 Blast Score: 195	Cyt_c_Oxidase_VIIa; Cytochrome c oxidase subunit VIIa. Cytochrome c oxidase (CcO), the terminal oxidase in the respiratory chains of eukaryotes and most bacteria, is a multi-chain transmembrane protein located in the inner membrane of mitochondria and the cell membrane of...

RNA

1. NR_029466.1 RNA Sequence

Description	Transcript Variant: This variant (2) uses an alternate splice site in an internal exon, compared to variant 1. This variant is represented as non-coding because the use of the supported translational start codon, as used in variant 1, renders the transcript a candidate for nonsense-mediated mRNA decay (NMD).
Source sequence(s)	AA878033,CR139775,CK821341

RefSeqs of Annotated Genomes: Build 37.1

The following sections contain reference sequences that belong to a specific genome build. Explain

Genome Reference Consortium Human Build 37 (GRCh37), Primary_Assembly

Genomic

1. NC_000006.11

Range	75947502..75953524, complement
Download	GenBank FASTA Sequence Viewer (Graphics)

2. NT_007299.13

Range 14067336..14073358, complement
Download | GenBank FASTA Sequence Viewer (Graphics)

Alternate assembly (Celera)

Genomic

1. AC_000049.1
   Range 76341237..76347257, complement
   Download | GenBank FASTA Sequence Viewer (Graphics)
2. NW_923184.1
   Range 8409841..8415861, complement
   Download | GenBank FASTA Sequence Viewer (Graphics)

Alternate assembly (HuRef)

Genomic

1. AC_000138.1
   Range 73146851..73152858, complement
   Download | GenBank FASTA Sequence Viewer (Graphics)
2. NW_001838987.1
   Range 5324853..5330860, complement
   Download | GenBank FASTA Sequence Viewer (Graphics)

Related Sequences

Nucleotides		Protein
Heading	Accession and Version	
genomic	AF134406.1	AAF61396.1
genomic	AL080250.11	CAI19899.1
genomic	CH471051.2	EAW48746.1
		EAW48747.1
mRNA	AA978033.1	None
mRNA	AK312154.1	BAG35088.1
mRNA	BC100852.1	AAI00853.1
mRNA	BC100853.1	AAI00854.1
mRNA	BC100854.2	AAI00855.1
mRNA	BC101826.1	AAI01827.1
mRNA	BC101828.1	AAI01829.1
mRNA	BC133654.1	AAI33655.1
mRNA	CB139775.1	None
mRNA	CK821341.1	None
mRNA	CR407646.1	CAG28574.1
mRNA	CR542125.1	CAG46922.1
mRNA	CR610116.1	None
mRNA	X16822.1	CAA33829.1

Protein Accession	Links	
	GenePept Link	UniProtKB Link
P14406.1	GenPept	UniProtKB/Swiss-Prot:P14406
Q49610	GenPept	UniProtKB/TrEMBL:Q49610

Additional Links

Additional Links

MIM 123996
UCSC UCSC
UniGene Hs.70312

Gene LinkOut

The following LinkOut resources are supplied by external providers. These providers are responsible for maintaining the links.

Medical
Molecular Biology Databases
Research Materials
Tools
Miscellaneous

Entrez Gene

Genes and mapped phenotypes

Display Settings: Full Report

NDUFAB1 NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa [*Homo sapiens*]

Gene ID: 4706, updated on 6-Aug-2010

Summary

Official Symbol	NDUFAB1 provided by HGNC
Official Full Name	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa provided by HGNC
Primary source	HGNC:7684
See related	Ensembl:ENSG00000004779; HPRD:11951; MIM:603836
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	ACP; SDAP; FASN2A; MGC65095; NDUFAB1

Genomic regions, transcripts, and products

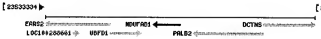
(minus strand) Go to reference sequence details

Go to nucleotide graphics

Genomic context

chromosome: 16; **Location:** 16p12.2

See NDUFAB1 in MapViewer



Bibliography

Related articles in PubMed

1. Association study between single-nucleotide polymorphisms in 199 drug-related genes and commonly measured quantitative traits of 752 healthy Japanese subjects. Saito A, *et al.* J Hum Genet, 2009 Jun. PMID 19343046.
2. Down-regulation of mitochondrial acyl carrier protein in mammalian cells compromises protein lipoylation and respiratory complex I and results in cell death. Feng D, *et al.* J Biol Chem, 2009 Apr 24. PMID 19221180.
3. Oxidative stress, telomere length and biomarkers of physical aging in a cohort aged 79 years from the 1932 Scottish Mental Survey. Starr JM, *et al.* Mech Ageing Dev, 2008 Dec. PMID 18977241.
4. Identification of a subunit of NADH-dehydrogenase as a p49/STRAP-binding protein. Zhang X, *et al.* BMC Cell Biol, 2008 Jan 29. PMID 18230186.
5. A genetic association analysis of cognitive ability and cognitive ageing using 325 markers for 109 genes associated with oxidative stress or cognition. Harris SE, *et al.* BMC Genet, 2007 Jul 2. PMID 17601350.

Exhibit B

See all (15) citations in PubMed

GeneRIFs: Gene References Into Functions What's a GeneRIF?

1. ACP has a dual role in mammalian mitochondrial function
2. Observational study of gene-disease association. (HuGE Navigator)
3. The p49/STRAP and NDUFAB1 proteins interacted and co-localized with each other in the cell.

Submit: New GeneRIF Correction

Phenotypes

Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls
NHGRI GWA Catalog

General gene information

Markers

RH64954 (e-PCR)
Links: UniSTS:92468
RH93191 (e-PCR)
Links: UniSTS:92725
SGC33525 (e-PCR)
Links: UniSTS:53405
G20300 (e-PCR)
Links: UniSTS:40905
A005L06 (e-PCR)
Links: UniSTS:40906
SHGC-32823 (e-PCR)
Links: UniSTS:17364

Genotypes

See NDUFAB1 SNP Geneview Report
See NDUFAB1 SNP Genotype Report

Pathways

KEGG pathway: Alzheimer's disease
05010
KEGG pathway: Huntington's disease
05016
KEGG pathway: Metabolic pathways
01100
KEGG pathway: Oxidative phosphorylation
00190
KEGG pathway: Parkinson's disease
05012
Reactome Event:Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.
REACT_6305

Gene Ontology provided by GOA

Function	Evidence	
	Evidence Code	Pubs
NADH dehydrogenase (ubiquinone) activity	NAS	PubMed
acyl carrier activity	NAS	PubMed
calcium ion binding	NAS	PubMed
cofactor binding	IEA	
fatty acid binding	ISS	
phosphopantetheine binding	IEA	

Evidence

Exhibit B

Process	Evidence Code	Pubs
electron transport chain	IEA	
fatty acid biosynthetic process	NAS	PubMed
mitochondrial electron transport, NADH to ubiquinone	NAS	PubMed
transport	IEA	

Component	Evidence	
	Evidence Code	Pubs
mitochondrial matrix	ISS	
mitochondrial membrane	ISS	
mitochondrial membrane	NAS	PubMed
mitochondrial respiratory chain complex I	IDA	PubMed
mitochondrial respiratory chain complex I	ISS	
mitochondrial respiratory chain complex I	NAS	PubMed
mitochondrion	IEA	
respiratory chain	IEA	

General protein information

Preferred Names
acyl carrier protein, mitochondrial

Names
acyl carrier protein, mitochondrial
CI-SDAP
complex I SDAP subunit
mitochondrial acyl carrier protein
NADH:ubiquinone oxidoreductase SDAP subunit
NADH-ubiquinone oxidoreductase 9.6 kDa subunit

NCBI Reference Sequences (RefSeq)

RefSeqs maintained independently of Annotated Genomes

These reference sequences exist independently of genome builds. Explain

mRNA and Protein(s)

1. NM_005003.2 → NP_004994.1 **acyl carrier protein, mitochondrial precursor**
   Source sequence(s): AF387060.BC029920.BI603093
   Consensus CDS: CCDS10614.1
   UniProtKB/Swiss-Prot: O14561
   Related Ensembl: ENSP00000007516, ENST00000007516, ENST00000484769
   Conserved Domains (1) **summary**
   cl09936: PP-binding, Phosphopantetheine attachment site
   Location:66 – 152
   Blast Score: 220

RefSeqs of Annotated Genomes: Build 37.1

The following sections contain reference sequences that belong to a specific genome build Explain

Genome Reference Consortium Human Build 37 (GRCh37), Primary_Assembly

Exhibit B

Genomic

1. NC_000016.9
   Range 23592334..23607638, complement
   Download GenBank FASTA Sequence Viewer (Graphics)

2. NT_010393.16
   Range 23532334..23547638, complement
   Download GenBank FASTA Sequence Viewer (Graphics)

Alternate assembly (Celera)

Genomic

1. AC_000059.1
   Range 22370507..22385818, complement
   Download GenBank FASTA Sequence Viewer (Graphics)

2. NW_926217.1
   Range 890711..905922, complement
   Download GenBank FASTA Sequence Viewer (Graphics)

Alternate assembly (HuRef)

Genomic

1. AC_000148.1
   Range 21682893..21697747, complement
   Download GenBank FASTA Sequence Viewer (Graphics)

2. NW_001838401.1
   Range 122652..137506, complement
   Download GenBank FASTA Sequence Viewer (Graphics)

Related Sequences

Nucleotide		Protein
Heading	Accession and Version	
genomic	AC002400.1	AAC05814.1
genomic	AC008870.6 (113247..126551)	None
genomic	CH471145.2	EAW55815.1
		EAW55816.1
mRNA	AF087660.1	AAD23566.1
mRNA	AK311877.1	BAG34818.1
mRNA	BC058920.1	AAH58920.1
mRNA	BI803093.1	None
mRNA	CR609167.1	None
mRNA	EF036490.1	ABQ59076.1

Protein Accession	Links	
	GenePept Link	UniProtKB Link
O14561.3	GenPept	UniProtKB/Swiss-Prot:O14561

Additional Links

Additional Links

Exhibit B

MIM 603636
UCSC UCSC
UniGene Hs.189716

Gene LinkOut

The following LinkOut resources are supplied by external providers. These providers are responsible for maintaining the links.

Molecular Biology Databases
Research Materials
Tools
Miscellaneous

Exhibit B